

Figure 1

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Figure 2a	
CCACAGGCAGCTCCCTGAAG(P O (A) G S S L K	598 61
	538
	478
, i	418
	358
	298
	238
AAAACTCCCTTTTAGCCCTCTGCCCCCCTTGCTTATAAGCCTTTGAGACCGCAGA	178
CCCCTTTTCCTTGAGAGACGAGTTGGGGGAGTCCTCCACGCATTACCCACTCGGGCCGCA	118
GGAGGCTGGTGGACACCCAGGCAGGGGGGGGGAAGAACTCTCTCCCTTTCTGAAC	58
r 1 Acceagggaaggaggcacaccegggggggggggcgcagtgagggggggggg	 1

8 11 11 31 31 31 31 31 31 31		3/19				
17 17 80	658 GAGGIGTCAGCTCCGGCCACCCTAGACTCCCTGTCCATCCACCAGCTCGCAGCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	GACGAGCGCGCTTCACCCCCTCATCTGGGCCTCATCTGGGCCTCATCTTGGCCAAAAGAGCGAGAGGCCCCCCCC	,	&	6	Figure 2b

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GAG	្រា
CIGA	വ
ACCC	۵
GCTG	A
BECAACCTGGTGCCCGC	വ
GIGC	>
IGG	H
SCC CCC	77.
SCA	S S
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,	117

TGAAGGCCGCCTGCCGGGGACTCAGACACTCAGGGAACAAATGGTCAGCCAGAGCTGGG

1258 GAAACCCAGAACTGACTTCAAAGGCAGCTTCTGGACAGGTGGTGGGAGGGGGACCCTTCCC

AAGAGGAACCAATAAACCTTCTGTGCAG - polya

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Figure 2c

60 35 29	1113 1119 87 81 25	170 170 179 144 138 80
MELTQPAEDLIQTQQTPASELGDPEDPGEEAADGSDTVVLSLFPCTPEPVNPEPDASVSS PVN-VPNP-VPD-ETRD-SPENDAA	HHHHT HHHHHHHHHT PQAGSSLKHSTTLTNRQRGNEVSALPATLDSLSIHQLAAQGELDQLKEHLRKG LF	TT HHHHHHHTH HHHHHHHHTTT TT TT HHHHHHHH
REXANK AREXANK b homol	SREXANK MREXANK s homol m homol	SREXANK IMREXANK S homol

Figure 3a

230 239 204 198	6/19
HHHHHHHTT TT TTT HHHHHHTT HHHHHHHHHHHH	HHTT HHHHHHH K VALGYRKVQQVIENHILKLFQSNLVPADPE 260 KM-SRT-G-V 269 1IEVFNRLLSHIC 1GCSDYMLVTDVFRI IDN-NEDLAEILQ
HSREXANK MmREXANK Hs homol Mm homol GABPβ	HSREXANK MMREXANK HS homol Mm homol

Figure 3b

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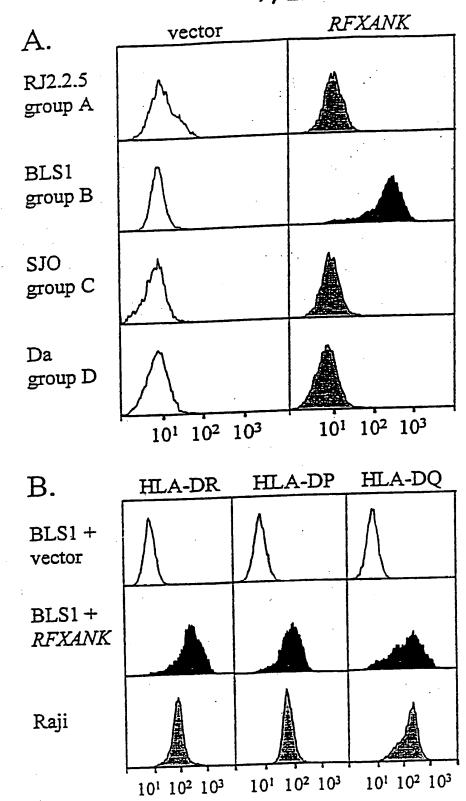
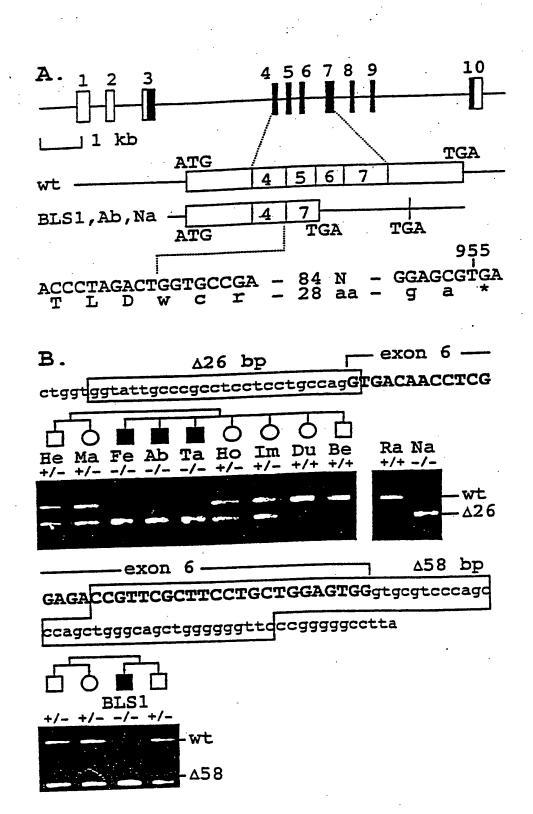
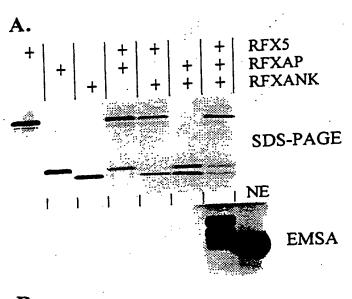


Figure 4



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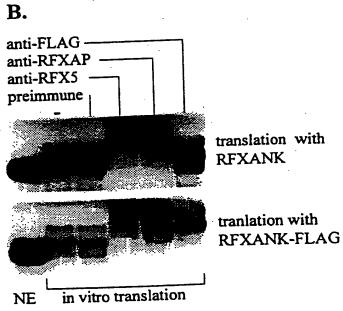


Figure 6

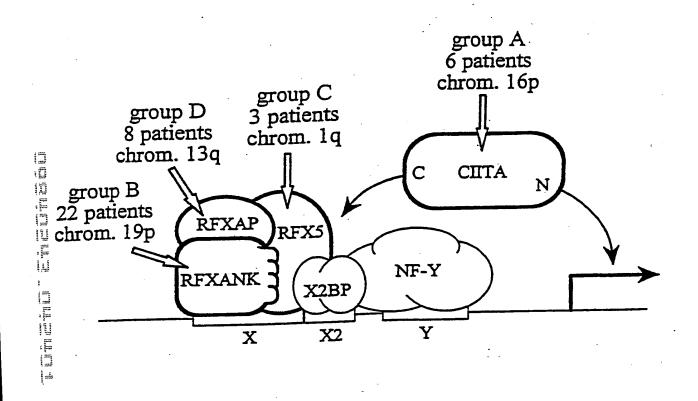


Figure 7

Figure 8

Figure 9



Figure 10a

extract:	SJO	STC)+RFX5
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RFX5			
NF_VR			

Figure 10b

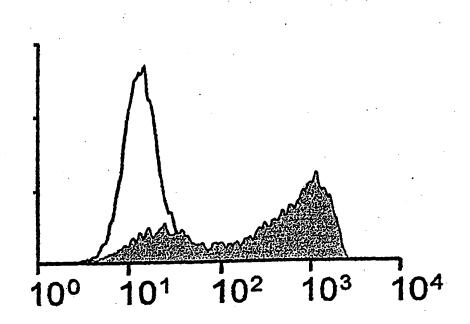


Figure 10c

Figure 11a

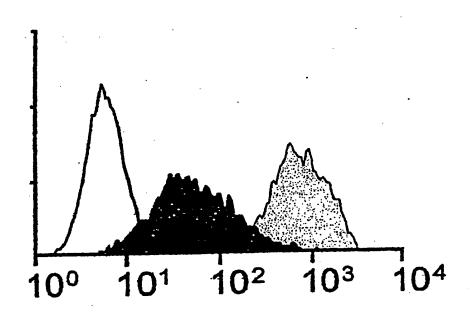


Figure 11b

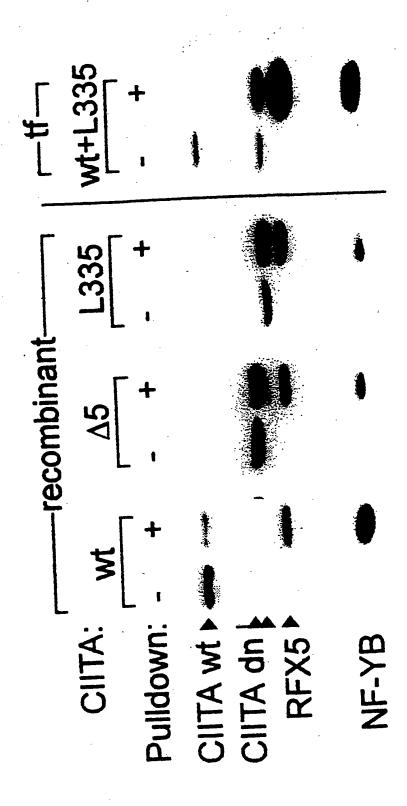


Figure 11c

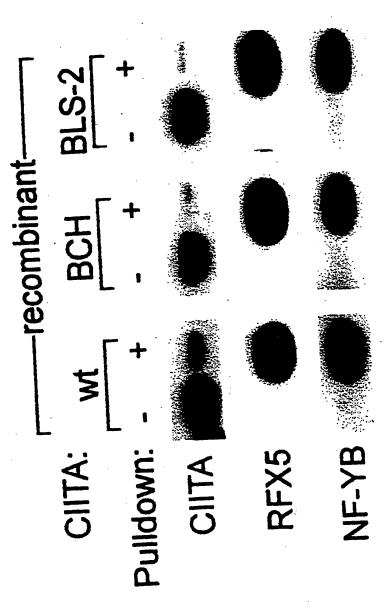


Figure 11d